

SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 (i) APPLICANT: Tsichlis, Philip
Grimes, H. Leighton III
Zweidler-McKay, Patrick
- 10 (ii) TITLE OF THE INVENTION: NUCLEIC ACID MOLECULE
FOR ENHANCING GENE EXPRESSION
- (iii) NUMBER OF SEQUENCES: 14
- 15 (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Dann, Dorfman, Herrell and
Skillman, P.C.
(B) STREET: 1601 Market Street, Suite 720
20 (C) CITY: Philadelphia
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19103-2307
- 25 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- 30 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: not assigned
(B) FILING DATE: 17-JUN-1997
(C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 60/019,808
(B) FILING DATE: 17-JUN-1996
- 40 (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Janet E. Reed
(B) REGISTRATION NUMBER: 36,252
(C) REFERENCE/DOCKET NUMBER:
- 45 (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (215) 563-4100
(B) TELEFAX: (215) 563-4044
(C) TELEX:
- 50 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 NAAATCACNG CA
12

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAAATCACNG CA
12

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(2) INFORMATION FOR SEQ ID NO:3:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NANNNNACNG CA
12

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(2) INFORMATION FOR SEQ ID NO:4:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 ANAAAAANAAA TCACNGCATA TGCC
24

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30 ACCATCACCA CATAAATCAC TGCCTATCCT GTG
33

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACCACATAA ATCACTGCCT ATCC
24

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(2) INFORMATION FOR SEQ ID NO:7:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 CACCACATAG ATCACTGCCT ATCC
24

(2) INFORMATION FOR SEQ ID NO:8:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 CACCACATAA CTCACTGCCT ATCC
24

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CACCACATAA ATAAC TGCCT ATCC
24

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(2) INFORMATION FOR SEQ ID NO:10:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10 CACCACATAA ATCAATGCCT ATCC
 24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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20 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 CACCACATAA ATCACTTCCT ATCC
 24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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40 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

50 GCCCGCCTGG CTGACCGCCC AACCACCCCC CGGGATTGAC GTCAATAATG ACGTATGTTC 60
 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGAGTAT TTACGGTAAA 120
 CTGCCCACCTT GGCAGTACAT CAAGTGTATC ATATGCCAAG TACGCCCCCT ATTGACGTCA 180
 ATGACGGTAA ATGGCCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA 240
 CTTGGCAGTA CATCTACGTA TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT 300
 ACATCAATGG GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTTG 360
 ACGTCAATGG GAGTTTGTTT TGGCACCAAA ATCAACGGGA CTTTCCAAAA TGTCGTAACA 420
 ACTCCGCCCC ATTGACGCAA ATGGGCGGTA GGCGTGTAAG GTGGGAGGTC TATATAAGCA 480
 55 GAGCTCGTTT AGTGAACCGT 500

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	GCCCCGCTGG	CTGACCGCCC	AACGACCCCC	CGGGATTGAC	GTCAATAATG	ACGTATGTTC	60
	CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	GGTGGAGTAT	TTACCCATAA	120
	CTGCCCCACTT	GGCAGTACAT	CAAGTGTAIC	ATATGCCAAG	TACGCCCCCT	ATTGACGTCA	180
20	ATGACGGTAA	ATGGCCCCGCC	TGGCATTATC	CCCACTACAT	GACCTTATGG	GACTTTCCCTA	240
	CTTGGCAGTA	CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCGG	TTTTGGCAGT	300
	ACATCAATGG	GCGTGGATAG	CGGTTTGACT	CACGGGGAGT	TCCAAGTCTC	CACCCCATTG	360
	ACGTCAATGG	GACTTTGTTT	TGGCACCAAA	CTCAACGGGA	CTTTCCAAAA	TGTCGTAACA	420
	ACTCCGCCCC	ATTGACGCAA	ATGGGCGGTA	GGCGTGACG	GTGGGAGGTC	TATATAAGCA	480
25	GAGCTCGTTT	AGTGAACCGT					500

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	GCCCCGCTGG	CTGACCGCCC	AACGACCCCC	CGGGATTGAC	GTCAATAATG	ACGTATGTTC	60
	CCATAGTAAC	GCCAATAGGG	ACTTTCCATT	GACGTCAATG	GGTGGAGTAT	TTACGGTAAA	120
45	CTGCCCCACTT	GGCAGTACAT	CAAGTGATATC	ATATGCCAAG	TACGCCCCCT	ATTGACGTCA	180
	ATGACGGTAA	ATGGCCCCGCC	TGGCATTATG	CCCACTACAT	GACCTTATGG	GACTTTCCCTA	240
	CTTGGCAGTA	CATCTACGTA	TTAGTCATCG	CTATTACCAT	GGTGATGCGG	TTTTGGCAGT	300
	ACATCAATGG	GCGTGGATAG	CGGTTTGACT	CACGGGACTT	TCCAAGTCTC	CACCCCATTG	360
	ACGTCAATGG	GAGTTTGTTT	TGGCACCAAA	ACTAACGGGA	CTTTCCAAAA	TGTCGTAACA	420
50	ACTCCGCCCC	ATTGACGCAA	ATGGGCGGTA	GGCGTGACG	GTGGGAGGTC	TATATAAGCA	480
	GAGCTCGTTT	AGTGAACCGT					500